

Figure 1

10 30 50  
 CACGCGTCCGCGGGCGCGGCCGCGGAGAACCCCGCAATCTTTGCGCCACAAAATACACCGA  
 70 90 110  
 CGATGCCCCGATCTACTTTAAGGGCTGAAACCCACGGGCCTGAGAGACTATAAGAGCGTTC  
 130 150 170  
 CCTACCGCCATGGAACAACGGGGACAGAACGCCCCGCGCTTCGGGGGCCCCGAAAAGG  
M E O R G O N A P A A S G A R K R  
 190 210 230  
 CACGGCCCAGGACCCAGGGAGGCGCGGGGAGCCAGGCCTGGGCCCCGGGTCCCCAAGACC  
H G P G P R E A R G A R P G P R V P K T  
 250 270 290  
 CTTGTGCTCGTTGTGCGCCGCGGTCTGCTGTTGGTCTCAGCTGAGTCTGCTCTGATCACC  
L V L V V A A V L L L V S A E S A L I T  
 310 330 350  
 CAACAAGACCTAGCTCCCCAGCAGAGAGCGGCCCCACAACAAAAGAGGTCCAGCCCCCTCA  
 Q Q D L A P Q Q R A A P Q Q K R S S P S  
 370 390 410  
 GAGGGATTGTGTCCACCTGGACACCATATCTCAGAAGACGGTAGAGATTGCATCTCTCTGC  
 E G L C P P G H H I S E D G R D C I S C  
 430 450 470  
 AAATATGGACAGGACTATAGCACTCACTGGAATGACCTCCTTTTCTGCTTGCCTGCACC  
 K Y G Q D Y S T H W N D L L F C L R C T  
 490 510 530  
 AGGTGTGATTGAGGTGAAGTGGAGCTAAGTCCCTGCACCACGACCAGAAACACAGTGTGT  
 R C D S G E V E L S P C T T T R N T V C  
 550 570 590  
 CAGTGCGAAGAAGGCACCTTCCGGGAAGAAGATTCTCCTGAGATGTGCCGGAAGTGCCGC  
 Q C E E G T F R E E D S P E M C R K C R  
 610 630 650  
 ACAGGGTGTCCCAGAGGGATGGTCAAGGTGCGGTGATTGTACACCCTGGAGTGACATCGAA  
 T G C P R G M V K V G D C T P W S D I E  
 670 690 710  
 TGTGTCCACAAAGAATCAGGCATCATATAGGAGTCACAGTTGCAGCCGTAGTCTTGATT  
 C V H K E S G I I I G V T V A A V V L I  
 730 750 770  
 GTGGCTGTGTTTGTGTTGCAAGTCTTTACTGTGGAAGAAAGTCCTTCCTTACCTGAAAGGC  
V A V F V C K S L L W K K V L P Y L K G  
 790 810 830  
 ATCTGCTCAGGTGGTGGTGGGGACCCTGAGCGTGTGGACAGAAGCTCACAACGACCTGGG  
 I C S G G G G D P E R V D R S S Q R P G  
 850 870 890  
 GCTGAGGACAATGTCCTCAATGAGATCGTGAGTATCTTGCAGCCCACCCAGGTCCCTGAG  
 A E D N V L N E I V S I L Q P T Q V P E  
 910 930 950  
 CAGGAAATGGAAGTCCAGGAGCCAGCAGAGCCAACAGGTGTCAACATGTTGTCCCCCGGG  
 Q E M E V Q E P A E P T G V N M L S P G  
 970 990 1010  
 GAGTCAGAGCATCTGCTGGAACCGGCAGAAGCTGAAAGGTCTCAGAGGAGGAGGCTGCTG  
 E S E H L L E P A E A E R S Q R R R L L  
 1030 1050 1070

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Figure 1 (continued)

GTTCAGCAAATGAAGGTGATCCCACTGAGACTCTGAGACAGTGCTTCGATGACTTTGCA  
V P A N E G D P T E T L R Q C F D D F A  
1090 1110 1130  
GACTTGGTGCCCTTTGACTCCTGGGAGCCGCTCATGAGGAAGTTGGGCCTCATGGACAAT  
D L V P F D S W E P L M R K L G L M D N  
1150 1170 1190  
GAGATAAAGGTGGCTAAAGCTGAGGCAGCGGGCCACAGGGACACCTTGACACGATGCTG  
E I K V A K A E A A G H R D T L Y T M L  
1210 1230 1250  
ATAAAGTGGGTCAACAAAACCGGGCGAGATGCCTCTGTCCACACCCTGCTGGATGCCTTG  
I K W V N K T G R D A S V H T L L D A L  
1270 1290 1310  
GAGACGCTGGGAGAGAGACTTGCCAAGCAGAAGATTGAGGACCACTTGTTGAGCTCTGGA  
E T L G E R L A K Q K I E D H L L S S G  
1330 1350 1370  
AAGTTCATGTATCTAGAAGGTAATGCAGACTCTGCCATGTCCTAAGTGTGATTCTCTTCA  
K F M Y L E G N A D S A M S \*  
1390 1410 1430  
GGAAGTGAGACCTTCCCTGGTTTACCTTTTTTCTGGAAAAAGCCCACTGGACTCCAGTC  
1450 1470 1490  
AGTAGGAAAGTGCCACAATTGTCACATGACCGGTACTGGAAGAACTCTCCCATCCAACA  
1510 1530 1550  
TCACCCAGTGGATGGAACATCCTGTAACCTTTTCACTGCACTTGGCATTATTTTTATAAGC  
1570 1590  
TGAATGTGATAATAAGGACACTATGGAAAAAAAAAAAAA

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Figure 2

1 M-LG- - - - - I W T L L P L V L L h Fas protein  
1 MGLS- - - - - T V P D L L L P L h TNFR I Protein  
1 MQR- - - - - P R G C A A V A A DR3 protein  
1 MQRG Q N A P A A S G A R K R H G P G P R E A R G A R P G P R V P K T L V L HLYBX88XXprotein

13 T S V A R L S S K S V N A Q V T D I N S K G L E L R K T V T T V E T Q N L E G L h Fas protein  
14 V L L E L L V G I Y P S G V I G L V P H L G D R E K R D S V C P Q G K Y I H - - h TNFR I Protein  
14 A L L E L L V L L G A R A Q G - - - - - G T R S P R - C D C A - G D F - H - - DR3 protein  
41 V V A A V E L L V S A E S A L I T Q Q D L A P Q Q R A A P Q Q K R S S P S E G L HLYBX88XXprotein

53 H E D G Q F C H K P C P P G E R K A R D C T V N G D E P D C V P C Q E G K E Y T h Fas protein  
52 P Q N N S I C C T K C H K G T Y L Y N D C P G P G Q D T D C R E C E S G S F T A h TNFR I Protein  
41 K K I G L F C C R G C P A G H Y L K A P C T E P C G N S T C L V C P Q D T F L A DR3 protein  
81 - - - - - C P P G H H I S E D - - - - - G R D C I S C K Y G Q D Y S HLYBX88XXprotein

93 D K A E F S S K C R R C R L C D E G H G L E V E I N C T R T Q N T K C R C K P N h Fas protein  
92 S E N H L R - H C L S C S K C R K Z M G Q V E I S S C T V D R D T V C G C R K N h TNFR I Protein  
81 W E N H H M S E C A R C Q A C D E Q A C S O V A L E N C S A V A D T R C G C K P G DR3 protein  
105 T E W N D L L F C C L R C T R C D - - - S E V E L S P C T T T R N T V C Q C E E G HLYBX88XXprotein

133 F F - - - - - C N S T V - - - C E H C D P C T K - - - - - L S C Q E h Fas protein  
131 Q Y R H Y W S E N L F Q C - - - - - F N C S L C L N - G T V H - - - - - L S C Q E h TNFR I Protein  
121 W F V E C - - - Q V S O C V S S S P F Y C Q P C L D C G A L H R H T R L L C S R DR3 protein  
143 T E R E - - - - - E D S P E M C R K C - - - - - R T G C P R HLYBX88XXprotein

149 - - - - - C E H G I I - - - K E C - - - - - T L T S N T K C K E - - - h Fas protein  
161 K Q N T V C T C H A G F F L R E N E C V S C S N C K K S I E C T F L C L P Q I E h TNFR I Protein  
158 R D T D C G T C L P G E Y Z H G D G C V S C P T S T L G - S C P E R C A A V C G DR3 protein  
163 G M V K V G D C T E - - - W S D I E C V - - - - - H K E S G I I I G HLYBX88XXprotein

168 - - - - - E G S R S N L G W - - - - - L C L L - L L P I P L I V - - - - - W h Fas protein  
201 N Y K G T E D S G T T V L L P L V I F F G L C L L S L L F I G L M Y R Y Q R - W h TNFR I Protein  
197 W R Q - - - - - M F W V Q V L L A G L V V P L L L G A T L T Y T Y R H C W DR3 protein  
189 - - - - - V T V A A V V L I V A V F - - - V C K S L L W K K V L P Y L K G I C S HLYBX88XXprotein

190 V E R E V Q K T C R R H F K E N Q G S H E S - - - - - h Fas protein  
240 - E S E L Y S I V C G R S T P E K E G E L E G T T T K P L A P N P S F S P T P G h TNFR I Protein  
229 - P H R P L - V F A D E A G M E A L T P P P A T H L S P L D S A H T L L A P P D DR3 protein  
221 - - - - - G G G G D P E R V D R S S Q R P G A E D N V L N E I V S I L Q E T Q HLYBX88XXprotein

213 - - - - - h Fas protein  
279 F T P T L G F S P V E S S T F T S S S T Y T P G D - C P N F A A P R R E V A P P h TNFR I Protein  
267 S S E K I C T V Q L V G N S W T P G Y B E T Q E A L C P Q V T W S W D Q L - - - E DR3 protein  
255 V P E Q E M E V O E P A E - - - - - P T G V N M L S P G - - - E S E H L - - - HLYBX88XXprotein

213 - - - - - P T L N P E T V A I N L - - - S D V D L S K Y I T T I A G V M h Fas protein  
313 Y Q G A D P I L A T A L A S D P I P N L Q K W E D S A H K P Q S L D T D D P A h TNFR I Protein  
305 S R A L G P A A A P T L S E - - - - - E S P A G S P A M M L Q P G B Q DR3 protein  
293 - - - - - L E P A E A E R S Q R R R L L V P A N E G D P T E T L R O HLYBX88XXprotein

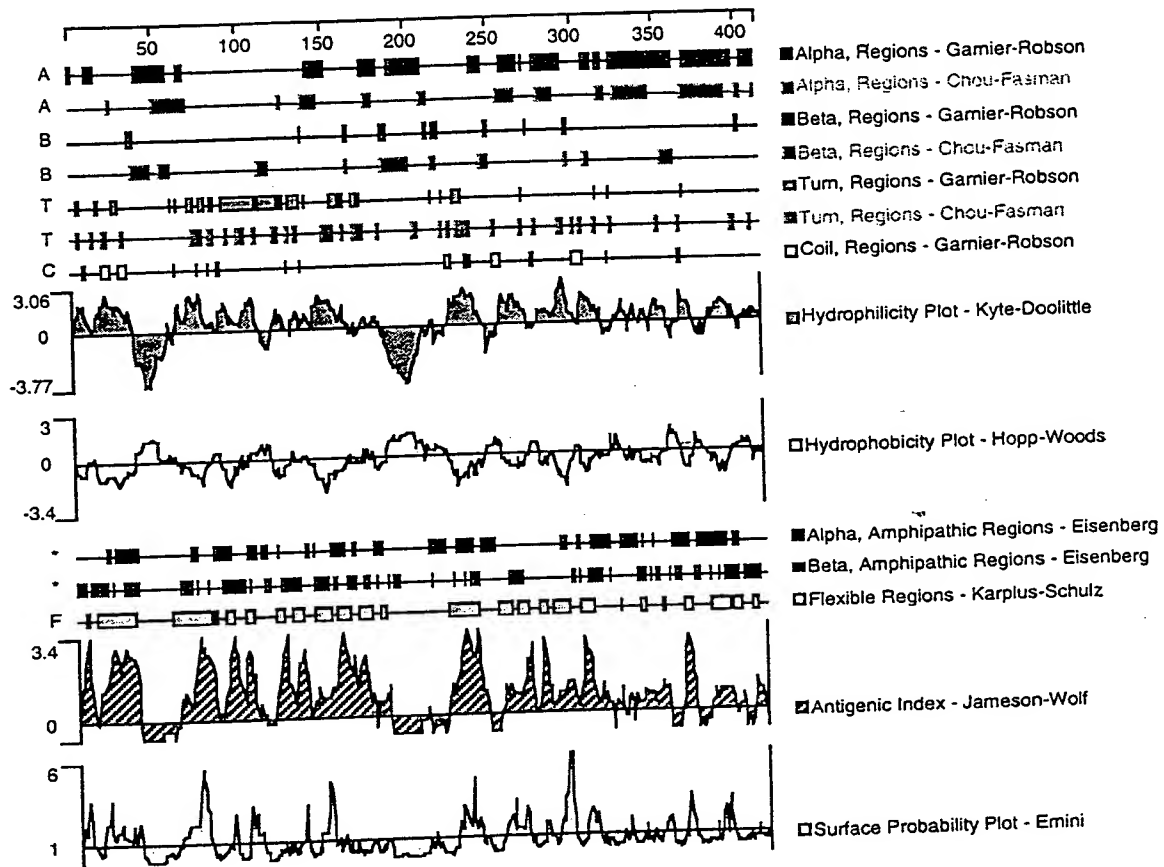
241 T L S Q V - - - - - K G F V R R N G V N E A K I D E I K N D N V Q D T A h Fas protein  
358 T L V A V V E N V P P L R W K E F V R R L G L S D H E I D R L E L Q N C R C L R h TNFR I Protein  
335 - L Y D V M D A V P A R R W K E F V R C L G L R E A E I E A V E V E I G R - F R DR3 protein  
312 C F D D F A D L V E F D S W E P L M R K L G L M D N E I - K V A K A E A A G H R HLYBX88XXprotein

272 E O K V Q L L R N U H O L H G K R E A - Y D T L I K D L K K A N L C T L A E K I h Fas protein  
398 E A Q Y S M L A T E R R R T P F R E A T L E L L G R V L R D M D L L G C L E D I h TNFR I Protein  
373 D O O Y E M L K R E R O Q Q P - - - A G L G A V Y A A L E R M G L D G C V E D L DR3 protein  
351 D T L Y T M L I K E V N K T G P - D A S V H T L L D A E L T L G E R L A K Q K I HLYBX88XXprotein

311 Q T I I E K D I T S D S E N S M F R N E I Q S L V h Fas protein  
438 E E A L - - - - - C G P A A L P P A P S L L R h TNFR I Protein  
419 - - - - - R S R L Q R G P DR3 protein  
390 E D H L L S S G K F M Y L E G M - - - A D S A M S HLYBX88XXprotein

Decorations: Decoration #1: Shade (with solid black) residues that match the Consensus exactly.

Figure 3



BB-TEO-EE524060

Figure 4

HAPBU13R

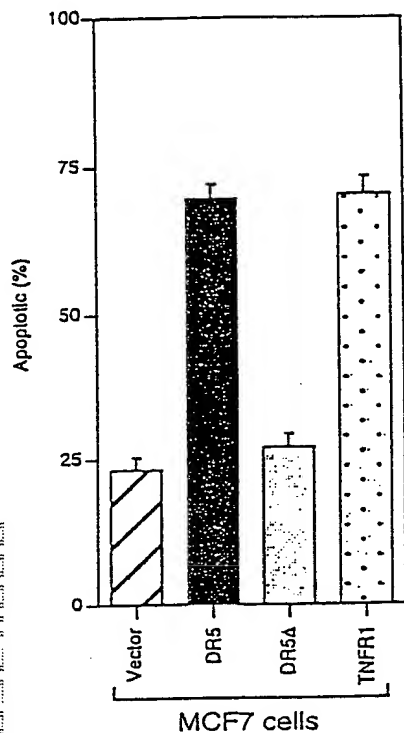
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51 TCTGGAAAAA GCCCAACTGG GACTCCAGTC AGTAGGAAAG TGCCACAATT  
101 GTCACATGAC CGGTACTGGA AGAAACTCTC CCATCCAACA TCACCCAGTG  
151 GNATGGGAAC ACTGATGAAC TTTTCACTGC ACTTGGCATT ATTTTTGTNA  
201 AGCTGAATGT GATAATAAGG GCACTGATGG AAATGTCTGG ATCATTCCGG  
251 TTGTGCGTAC TTTGAGATTT GNGTTTGGGG ATGTNCATTG TGTTTGACAG  
301 CACTTTTTTN ATCCCTAATG TNAAATGCNT NATTTGATTG TGANTTGGGG  
351 GTNAACATTG GTNAAGGNTN CCCNTNTGAC ACAGTAGNTG GTNCCC GACT  
401 TANAATNGNN GAANANGATG NATNANGAAC CTTTTTTTGG GTGGGGGGGT  
451 NNCGGGGCAG TNNAANGNNG NCTCCCCAGG TTTGGNGTNG CAATNGNGGA  
501 ANNNTGG

HSBBU76R

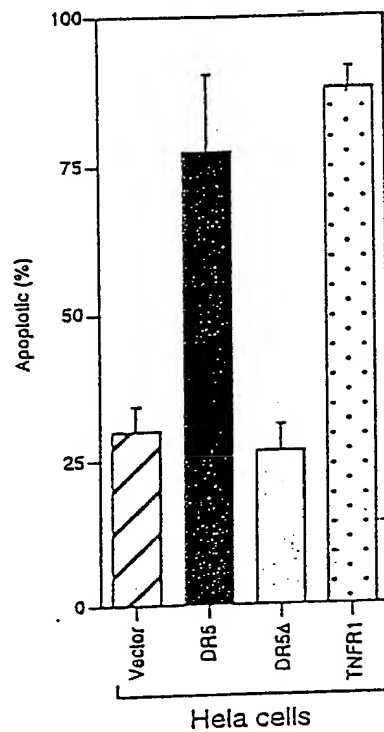
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51 ATTTACATTA GGATAAAAAA GTGCTGTGAA AACAATGACA TCCCAAACCA  
101 AATCTCAAAG TACGCACAAA CGGAATGATC CAGACATTTC CATAGNGTCC  
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201 ACAGGATGTT CCATCCACTG GGTGGATT

Figure 5

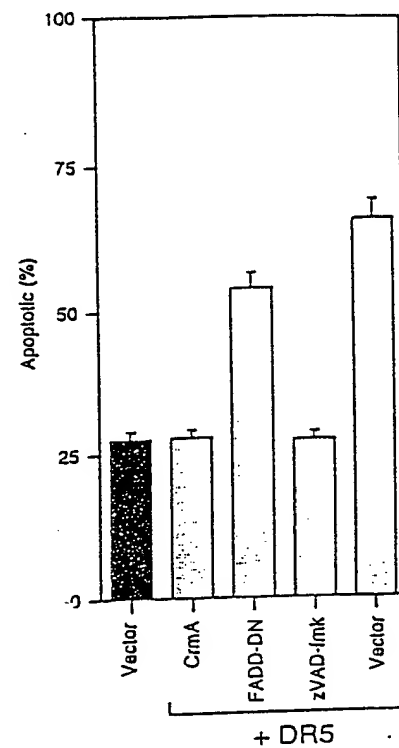
A



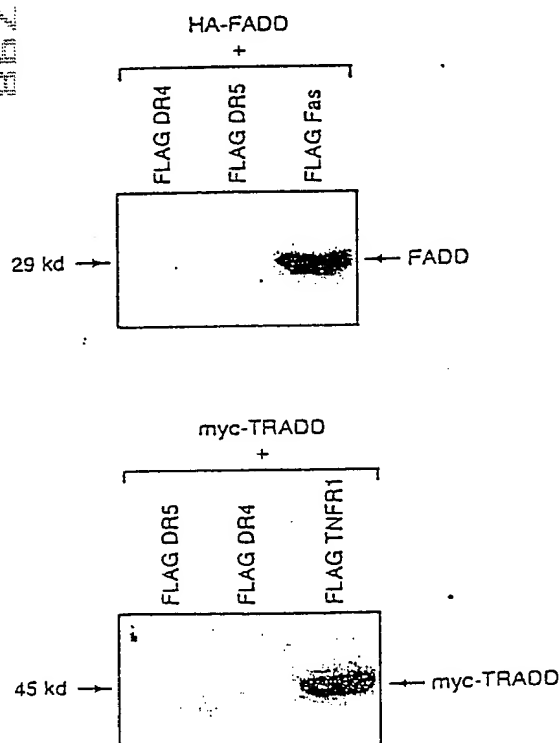
B



C



D



E

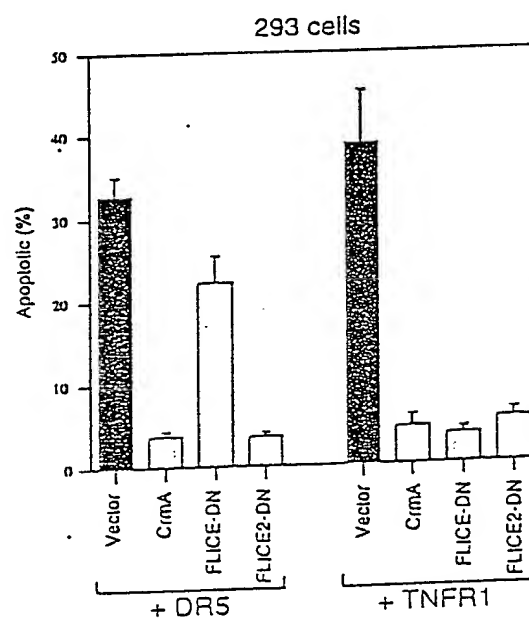
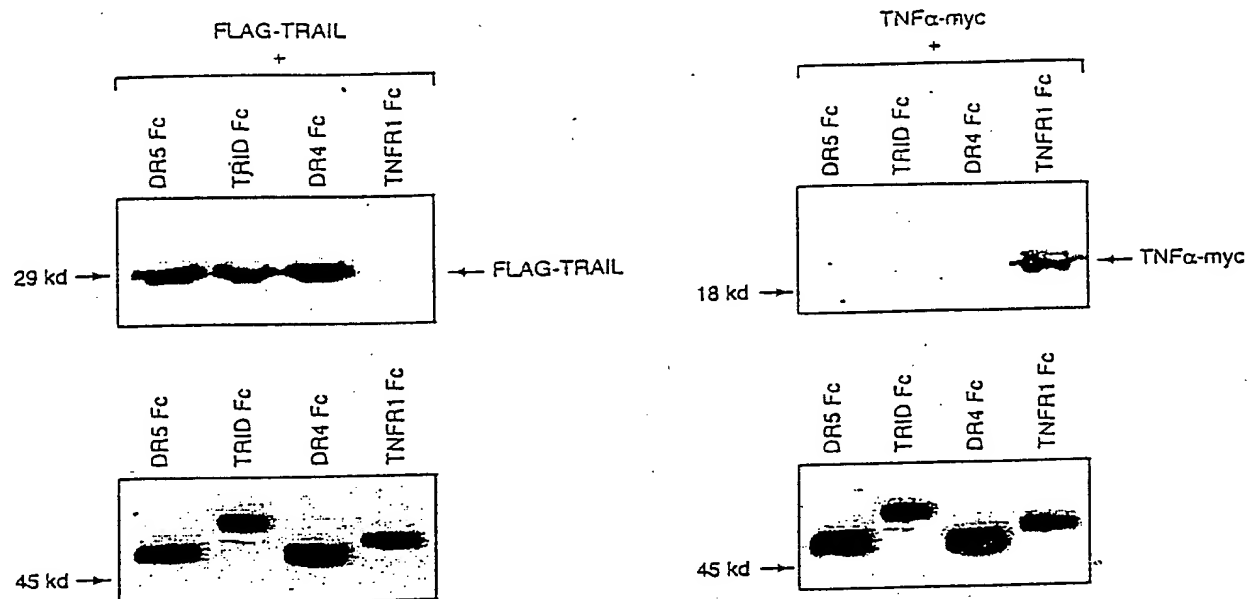
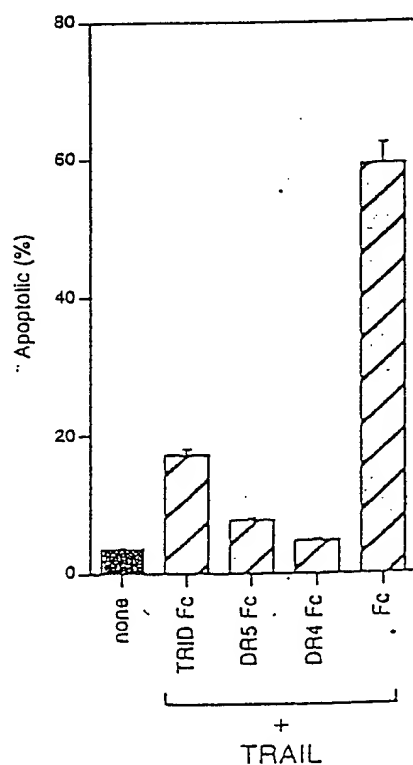


Figure 6

A



B



C

